

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2004, 19:35:16 ; Search time 17:0625 Seconds
 (without alignment) ;
 39.474 Million cell updates/sec

Title: US-10-618-644-2

Perfect score: 42

Sequence: 1 PNNKPFQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0¹

Database : PIR_79;*
 1: PIR;*
 2: PIR;*
 3: PIR;*
 4: PIR;*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	481	2 S04605	glycinin G3 - soy
2	42	100.0	484	2 S11003	glycinin G3 precur
3	42	100.0	485	1 FWSYG1	glycinin chain A2B
4	42	100.0	485	2 S11002	glycinin G2 precur
5	42	100.0	495	1 FWSYG2	glycinin chain A1a
6	42	100.0	495	2 S10851	glycinin G1 precur
7	42	100.0	565	1 HMIV61	hemagglutinin prec
8	37	88.1	330	2 JQ2375	hemagglutinin - in
9	37	88.1	330	2 JQ2374	hemagglutinin - in
10	37	88.1	331	2 JQ2378	hemagglutinin - in
11	37	88.1	331	2 JQ2377	hemagglutinin - in
12	37	88.1	347	2 S52186	hemagglutinin - in
13	37	88.1	347	2 S52175	hemagglutinin - in
14	37	88.1	347	2 S52187	hemagglutinin - in
15	37	88.1	347	2 S52183	hemagglutinin - in
16	37	88.1	347	2 S52180	hemagglutinin - in
17	37	88.1	347	2 S52182	hemagglutinin - in
18	37	88.1	347	2 S52179	hemagglutinin - in
19	37	88.1	347	2 S52198	hemagglutinin - in
20	37	88.1	347	2 S52185	hemagglutinin - in
21	37	88.1	347	2 S52189	hemagglutinin - in
22	37	88.1	347	2 S52191	hemagglutinin - in
23	37	88.1	347	2 S52199	hemagglutinin - in
24	37	88.1	347	2 S52178	hemagglutinin - in
25	37	88.1	347	2 S52188	hemagglutinin - in
26	37	88.1	347	2 S52173	hemagglutinin - in
27	37	88.1	347	2 S52174	hemagglutinin - in
28	37	88.1	347	2 S52195	hemagglutinin - in
29	37	88.1	347	2 S52197	hemagglutinin - in

ALIGNMENTS

RESULT 1						
S04605	Glycinin G3 - soybean	C;Species: Glycine max (soybean)	C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004			
		C;Accession: S04605				
		R;Cho, T.J.; Nielsen, N.C.				
		Nucleic Acids Res. 17, 4388, 1989				
		A;Title: The glycinin Gy(3) gene from soybean.				
		A;Reference number: S04605; MUID:8929500; PMID:2740231				
		A;Molecule type: DNA				
		A;Residues: 1-481 <CHO>				
		A;Cross-references: UNIPROT:P11828; EMBL:X15123; PIDN:CAA33217.1; PMID:918638; PIDN:CAA33217.1; PMID:91863				
		A;Experimental source: variety dare				
		C;Genetics:				
		A;Gene: Gy3				
		A;Introns: 96/1; 177/3; 352/3				
		C;Superfamily: glycinin				
Query	Match	Best Local Similarity	Score 42;	DB 2;	Length 481;	
Qy	1 PNNKBFQ	100.0%	Score 42;	DB 2;	Length 481;	
		100.0%	Prod. No. 1.3;			
		0; Mismatches 0;	Indels 0;			
		Gaps 0;				
RESULT 2						
S11003	Glycinin G3 precursor - soybean	C;Species: Glycine max (soybean)	C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 03-May-1996			
		C;Accession: S11003				
		R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thath, V.H.; Scallon, B.J.; Fischer, R.L.				
		Plant Cell 1, 313-328, 1989				
		A;Title: Characterization of the glycinin gene family in soybean.				
		A;Reference number: S10851; MUID:92393391; PMID:2485233				
		A;Accession: S11003				
		A;Molecule type: DNA				
		A;Residues: 1-484 <NIKE>				
		A;Experimental source: variety dare				
		C;Genetics:				
		A;Gene: Gy3				
		C;Superfamily: Glycinin				
		C;Keywords: storage protein				
		F;1-19/Domain: signal sequence #status predicted <SIG>				
		F;20-484/Product: glycinin G3 #status predicted <MAT>				
		Query Match	100.0%	Score 42;	DB 2;	Length 484;
		Best Local Similarity	100.0%	Prod. No. 1.3;		

Matches	7	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Qy	1 PNNKPFQ 7 								
Db	57 PNNKPFQ 63 								
RESULT 3									
PNSYGI Glycinin chain A2B1a precursor - soybean									
N:Alternate names: 11S globulin - N:Contents: Glycinin chain A2; glycinin chain B1a									
C:Species: Glycine max (soybean)									
C:Accession: A91341; E92454; A90024; A92452; S10503; S74123; A05164; A05 R/Momma, T.; Negoro, T.; Ueda, K.; Fukazawa, C.									
PEBS Lett. 188, 117-122, 1985									
A:Title: A complete cDNA Coding for the sequence of glycinin A2B1a subunit precursor.									
A:Reference number: A91341									
A: Molecule type: mRNA									
A:Residues: 1-485 <M1>									
A:Cross-references: UNIPROT:P04405									
A:Experimental source: strain Bonnimmori									
A:Note: the source of this mRNA was cotyledon tissue taken from seeds at the middle stage of development.									
R/Marco, T.; Thanh, N.E.; Scallan, B.J.; Nielsen, N.C.									
J. Biol. Chem. 259, 13416-13441, 1984									
A:Title: Cloning and structural analysis of DNA encoding an A2B1a subunit of glycinin.									
A:Accession: A92454									
A: Molecule type: mRNA									
A:Accession: B92454									
A:Residues: 3-485 <M2>									
A:Experimental source: strain CX635-1-1-1.									
R/Uesumi, S.; Kim, C.S.; Kohno, M.; Kito, M.									
Agric. Biol. Chem. 51, 3267-3273, 1987									
A:Title: Polymorphism and expression of cDNAs encoding glycinin subunits.									
A:Reference number: A90024									
A:Accession: A90024									
A:Molecule type: DNA									
A:Residues: 1-38 'D', 40-485 <M2>									
A:Experimental source: strain Shirotsurunoko									
R/Staswick, P.E.; Hermrodson, M.A.; Nielsen, N.C.									
J. Biol. Chem. 259, 13242-13430, 1984									
A:Title: The amino acid sequence of the A2B1a subunit of glycinin.									
A:Reference number: A92452; PMID:85030470; PMID:6541652									
A: Molecule type: protein									
A:Residues: 19-38, 'D', 10-60, 'S', '62-116, 'C', '118-192, 'E', '194-296-301-342, 'S', '344-463, 'I', '4									
A:Experimental source: strain CK35-1-1-1									
A:Note: residues 94-Gly, 103-Glu, 318-Thr, 331-Val, 400-Asp and 400-Arg, 409-Val									
polypeptides differing slightly in their primary sequences									
R/Staswick, P.E.; Hermrodson, M.A.; Nielsen, N.C.									
J. Biol. Chem. 259, 13431-13435, 1984									
A:Title: Identification of the cysteines which link the acidic and basic components of the									
A:Reference number: A92453; PMID:85030471; PMID:6541653									
A:Contents: annotation: disulfide bond									
R/Kitamura, Y.; Arahira, M.; Itoh, Y.; Fukazawa, C.									
Nucleic Acids Res. 18, 4245, 1990									
A:Title: The complete nucleotide sequence of soybean glycinin A2B1a gene spanning to and									
A:Reference number: S10502; PMID:90332420; PMID:2377465									
A:Status: translation not shown									
A:Molecule type: DNA									
A:Residues: 1-3 'K1P'									
A:Cross-references: EMBL:X53404; NID:918522; PIDN:CAA37480-1; PID:918524									
R/Shutov, A.D.; Kakhorskaya, I.A.; Bastrigina, A.S.; Bulmaga, V.P.; Horstmann, C.; Muend									
EU: J. Biotech. 241, 221-228, 1996									
A:Title: Limited proteolysis of beta-conglycinin and Glycinin, the 7S and 11S storage gl									
A:Reference number: S74123; MUID:90332420; PMID:8838910									
A:Accession: S74123									
RESULT 4									
S11002 glycinin G2 precursor - soybean									
N:Alternate names: Glycinin A2B1a									
C:Species: Glycine max (soybean)									
C:Accession: A91341; E92454; A90024; A92452; S10503; S74123; A05164; A05									
Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 7; Conservative 0; Gaps 0; Indels 0;									
Qy 1 PNNKPFQ 7 Db 54 PNNKPFQ 60									
RESULT 5									
S11002 glycinin G2 precursor - soybean									
N:Alternate names: Glycinin A2B1a									
C:Species: Glycine max (soybean)									
C:Accession: S11002; S04604; A26990									
Plant Cell 1, 213-229, 1989									
A:Title: Characterization of the glycinin gene family in soybean.									
A:Reference number: S10851; MUID:89239391; PMID:2485233									
A: Molecule type: DNA									
A:Residues: 1-485 <N1E>									
A:Experimental source: variety Dare									
R/Fukazawa, C.; Momma, T.; Higuchi, W.; Ueda, K.									
Nucleic Acids Res. 15, 8117, 1987									
A:Title: Complete nucleotide sequence of the gene encoding a glycinin A2B1a subunit pre-									
A:Accession: A26990									
A: Molecule type: DNA									
A:Residues: 1-485 <PTK>									
A:Experimental source: variety Dare									
R/Fukazawa, C.; Momma, T.; Higuchi, W.; Ueda, K.									
Nucleic Acids Res. 15, 8117/3, 356/3									
A:Title: Complete nucleotide sequence of the gene encoding a glycinin A2B1a subunit pre-									
A:Accession: A26990									
A: Molecule type: DNA									
A:Residues: 1-485 <PTK>									
A:Experimental source: variety Dare									
R/Fukazawa, C.; Momma, T.; Higuchi, W.; Ueda, K.									
Nucleic Acids Res. 15, 8117/3, 356/3									
A:Title: Complete nucleotide sequence of soybean glycinin A2B1a gene spanning to and									
A:Reference number: S10502; PMID:90332420; PMID:2377465									
A:Status: translation not shown									
A:Molecule type: DNA									
A:Residues: 1-3 'K1P'									
A:Cross-references: EMBL:X53404; NID:918522; PIDN:CAA37480-1; PID:918524									

RESULT 5

PFNYG2
Glycinin chain AlaBx precursor - soybean
N:Alternative names: 11S globulin; Glycinin AlaBb
C:Species: Glycine max (soybean)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

A:Accession: A23497; S10502
R:Negoro, T.; Momma, T.; Fukazawa, C.
Nucleic Acids Res. 13, 6719-6731, 1985
A:Title: A cDNA clone encoding a glycinin A-1a subunit precursor of soybean.
A:Reference number: A23497; MUID:86041867; PMID:2997720
A:Accession: A23497
A:Molecule type: mRNA
A:Residues: 1-495 <KIT>
A:Cross-references: UNIPROT:P04776; GB:X02985; NID:918614; PID:CAA26723.1; PID:918615
A:Experimental source: cv. Bonmimori
A:Note: the authors translated the codon AAC for residue 449 as Lys
A:Note: because of current nomenclature ambiguities, the authors choose to designate the R:Kitamura, Y.; Arahama, M.; Itoh, Y.; Fukazawa, C.
Nucleic Acids Res. 18, 4245, 1990
A:Title: The complete nucleotide sequence of soybean glycinin A2B1a gene spanning to and A:Accession: S10502; MUID:90332420; PMID:2377465
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 481-495 <KIT>
A:Cross-references: EMBL:X53404; NID:918522; PID:CAA37479.1; PID:918523
C:Comment: The source of this protein was cotyledon tissue taken 38 days after flowering
C:Comment: By homology with the A2B1a component, residues 307-310, and 491-495 are removed
C:Superfamily: Glycinin
C:Keywords: seed; storage protein
F:1-19/Domain: signal sequence #status predicted <GLA>
F:20-306/Product: glycinin chain Ala #status predicted <GLB>
F:311-490/Product: glycinin chain Bx #status predicted
F:107-317/Disulfide bonds: #status predicted

Query Match 100.0% Score 42; DB 1; Length 495;
Best Local Similarity 100.0% Pred. No. 1.3; 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
Db 57 PNNKPFQ 63

RESULT 7

HM16EV1
hemagglutinin precursor - influenza A virus (strain A/equine/Uruguay/1/63 [H3N81])
N:Contains: hemagglutinin HA1; hemagglutinin HA2
C:Species: influenza A virus
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
C:Accession: A34064
R:Kawachi, Y.; Bean, W.J.; Webster, R.G.
Virology 169, 283-292, 1989
A:Title: Evolution of the hemagglutinin of equine H3 influenza viruses.
A:Reference number: A34064; MUID:89203899; PMID:2705299
A:Accession: A34064
A:Molecule type: genomic RNA
A:Residues: 1-565 <KA>
A:Cross-references: GB:M24718; GB:J04336; NID:9124024; PID:9124024; PID:g324025
C:Genetics:
A:Map position: segment 4
C:SuperFamily: influenza virus hemagglutinin
C:Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thioester bond
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-344/Product: hemagglutinin HA1 #status predicted <HA1>
F:345-565/Product: hemagglutinin HA2 #status predicted <HA2>
F:535-551/Domain: transmembrane #status predicted <TM1>
F:29-481,67-292,79-91,154-488,295-320/Disulfide bonds: #status predicted
F:37-53,78,180,300,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 100.0% Score 42; DB 1; Length 565;
Best Local Similarity 100.0% Pred. No. 1.5; 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
Db 304 PNNKPFQ 310

RESULT 8

JQ275
hemagglutinin - influenza A virus (strain SN1389 and IN0190)
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JQ2375; JQ2376
R:Rocha, B.P.; Xu, X.; Hall, H.B.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A:Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A:Reference number: JQ2369; MUID:94065682; PMID:8245870
A:Accession: JQ2375

A; Molecule type: mRNA
 A; Residues: 1-330 <ROC>
 A; Cross-references: UNIPROT:Q7LZX9; GB:L20119
 A; Experimental source: subtype H3N2
 C; Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 330;
 Best Local Similarity 85.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
 Db 290 PNDKPFQ 296

RESULT 9
 JQ2374 hemagglutinin - influenza A virus (strain SN1289)
 C; Species: influenza A virus
 C; Accession: JQ2374
 R.; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
 A; Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
 A; Reference number: JQ2369; MUID:94065682; PMID:8245870
 A; Cross-references: UNIPROT:Q7LZX0; GB:L20115
 A; Experimental source: subtype H3N2
 C; Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 330;
 Best Local Similarity 85.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
 Db 290 PNDKPFQ 296

RESULT 10
 JQ2378 hemagglutinin - influenza A virus (strain HI0191)
 C; Species: influenza A virus
 C; Accession: JQ2378
 R.; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
 A; Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
 A; Reference number: JQ2369; MUID:94065682; PMID:8245870
 A; Cross-references: UNIPROT:Q7LZX7; GB:L20102
 A; Experimental source: subtype H3N2
 C; Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 331;
 Best Local Similarity 85.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
 Db 291 PNDKPFQ 297

RESULT 11
 JQ2377 hemagglutinin - influenza A virus (strain SD0191)
 C; Species: influenza A virus
 C; Accession: JQ2377
 R.; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
 A; Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
 A; Reference number: JQ2369; MUID:94065682; PMID:8245870
 A; Cross-references: UNIPROT:Q7LZX8; GB:L20105
 A; Experimental source: subtype H3N2
 C; Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 331;
 Best Local Similarity 85.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
 Db 291 PNDKPFQ 297

RESULT 12
 SS2186 hemagglutinin - influenza A virus (isolate A/England/68/94) (fragment)
 C; Species: influenza A virus
 C; Accession: SS2186
 R.; Ellis, J.S.
 A; Description: Antigenic and genetic variation in the haemagglutinin of recently
 A; Reference number: SS2173
 A; Cross-references: UNIPROT:QB2785; EMBL:Z46404; NID:9609045; PIDN:CAA86539.1; PI
 A; Experimental source: isolate A/England/68/94
 C; Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 347;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
 Db 289 PNDKPFQ 295

RESULT 13
 SS2175 hemagglutinin - influenza A virus (isolate A/England/1/93) (fragment)
 C; Species: influenza A virus
 C; Accession: SS2175
 R.; Ellis, J.S.
 A; Description: Antigenic and genetic variation in the haemagglutinin of recently
 A; Reference number: SS2173
 A; Cross-references: UNIPROT:QB2775; EMBL:Z46393; NID:9609024; PIDN:CAA86528.1; PI
 A; Experimental source: isolate A/England/1/93
 C; Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 347;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
 Db 289 PNDKPFQ 295

RESULT 14
 S52187 hemagglutinin - influenza A virus (isolate A/England/7/94) (fragment)
 C;Species: influenza A virus
 A;Variety: isolate A/England/7/94
 C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C;Accession: S52187
 R;Ellis, J. S.
 Submitted to the EMBL Data Library, October 1994
 A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula
 A;Reference number: S52173
 A;Accession: S52187
 A;Molecule type: mRNA
 A;Residues: 1-347 <BL>
 A;Cross-references: UNIPROT:Q82786; EMBL:Z46405; NID:9609047; PIDN:CAA86540.1; PID:96090
 A;Experimental source: isolate A/England/7/94
 C;Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 347;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PNNKPFQ 7
 Db 289 PNDKPFQ 295

RESULT 15
 S52183 hemagglutinin - influenza A virus (isolate A/England/347/93) (fragment)
 C;Species: influenza A virus
 A;Variety: isolate A/England/347/93
 C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C;Accession: S52183
 R;Ellis, J. S.
 Submitted to the EMBL Data Library, October 1994
 A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula
 A;Reference number: S52173
 A;Accession: S52183
 A;Molecule type: mRNA
 A;Residues: 1-347 <BL>
 A;Cross-references: UNIPROT:Q82782; EMBL:Z46401; NID:9609039; PIDN:CAA86536.1; PID:96090
 A;Experimental source: isolate A/England/347/93
 C;Superfamily: influenza virus hemagglutinin

Query Match 88.1%; Score 37; DB 2; Length 347;
 Best Local Similarity 85.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PNNKPFQ 7
 Db 289 PNDKPFQ 295

Search completed: November 6, 2004, 19:54:12
 Job time : 18.0625 secs

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